

SEQUENCE LISTING

<110> Large Scale Biology Corporation
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<120> PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT EXPRESSION

<130> LSBC-0087-CP09B

<150> 09/993,059

<151> 2001-11-13

<150> 09/626,127

<151> 2000-07-26

<150> 09/316,572

<151> 1999-05-21

<150> 08/324,003

<151> 1994-10-14

<150> 08/176,414

<151> 1993-12-29

<150> 07/997,733

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<150> 07/600,244

<151> 1990-10-22

<150> 07/641,617

<151> 1991-01-16

<150> 07/737,899

<151> 1991-07-26

<150> 07/739,143

<151> 1991-08-01

<150> 07/310,881

<151> 1989-02-17

<150> 07/160,766

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<150> 07/160,771

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<150> 07/347,637
<151> 1989-05-05

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<151> 1989-06-08

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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
35 40 45

Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
50 55 60

Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
65 70 75 80

Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
85 90 95

Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
100 105 110

Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu
115 120 125

Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
130 135 140

Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
145 150 155 160

Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
210 215 220

Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
245 250 255

Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
260 265 270

Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
275 280 285

Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
290 295 300

Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln

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Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met			
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Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val			
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Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr			
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Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser			
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gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta	360
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gcagatgggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac	600

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Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg

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Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
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Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
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 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
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Asp Glu Leu
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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
 35 40 45

Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
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Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
 65 70 75 80

Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
 85 90 95

Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
 100 105 110

Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu
 115 120 125

Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
 130 135 140

Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
 145 150 155 160

Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
 165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
 180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
 195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
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Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
 225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
 245 250 255

Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
 260 265 270

Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
 275 280 285

Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
 290 295 300

Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln
 305 310 315 320

Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe
 325 330 335

Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met
 340 345 350

Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val
 355 360 365

Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr
 370 375 380

Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser
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Glu Asn Thr Met Gln Met Ser Leu
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Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
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Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu
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gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggt 1080
ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct 1140
gcctgcttca tcacacagct cctccctgtg aaaaggaagc taggggttcta tgaatggact 1200
tcaagggttaa gaagtcacat aaatcccaca ggcactgttt tgcttcagct agaaaacaca 1260
atgtaa 1266

<210> 12
<211> 421
<212> PRT
<213> Homo sapiens

<400> 12

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
1 5 10 15

Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile

370

375

380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

Leu Glu Asn Thr Met
 420

<210> 13
 <211> 1284
 <212> DNA
 <213> Homo sapiens

<400> 13
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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgccca ggaagagcca 180
 gattcctgca tcagtgcaga gctcttcatg gagatggcag agctcatggc ctcagaaggc 240
 tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300
 gattcagaag gcagacttca ggcagacctt cagcgctttc ctcatgggat tcgccagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggatgt atgcagatgt tggaaataaa 420
 acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgccca gacctttgct 480
 gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tcctgtgagt ggctcttcta tatgtggccc ttccaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
 ggttggaaatg acccagatat gttagtgtat ggcaactttg gcctcagctg gaatcagcaa 840
 gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
 cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
 caggaccctt tgggcaagca aggggtaccag cttagacagg gagacaactt tgaagtgtgg 1020
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 gcctgcttca tcacacagct cctccctgtg aaaaggaagc taggggttcta tgaatggact 1200
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 atgtctgaaa aggacgaatt atga 1284

<210> 14
 <211> 427
 <212> PRT
 <213> Homo sapiens

<400> 14

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
 1 5 10 15

Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser

165	170	175
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn		
180	185	190
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met		
195	200	205
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn		
210	215	220
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys		
225	230	235
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val		
245	250	255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn		
260	265	270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala		
275	280	285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser		
290	295	300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn		
305	310	315
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn		
325	330	335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala		
340	345	350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala		
355	360	365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile		
370	375	380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr		
385	390	395
		400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
405 410 415

Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu
420 425

<210> 15
<211> 1254
<212> DNA
<213> Homo sapiens

<400> 15
atgcagctga ggaaccacaga actacatctg ggctgcgcgc ttgcgcttcg cttcctggcc 60
ctcgttttcct gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct 120
accatgggct ggctgcactg ggagcgcctc atgtgcaacc ttgactgcca ggaagagcca 180
gattcctgca tcagtgagaa gctcttcatt gagatggcag agctcatggc ctcagaaggc 240
tggaaggatg cagggttatga gtacctctgc attgatgact gttggatggc tcccaaaga 300
gattcagaag gcagacttca ggcagacctc cagcgccttc ctcattggat tcgccagcta 360
gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
acctgcgcag gcttcctctg gagttttgga tactacgaca ttgatgcca gacctttgct 480
gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540
gcagatgggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
tcctgtgagt ggccctctta tatgtggccc ttccaaaagc ccaattatac agaaatccga 660
cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840
gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
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ggacctcgct cttataccat cgcagttgct tccttgggta aaggagtggc ctgtaatcct 1140
gcctgcttca tcacacagct cctccctgtg aaaaggaagc taggggttcta tgaatggact 1200
tcaagggtta gaagtacat aaatcccaca ggcactggtt tgcttcagct ataa 1254

<210> 16
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
 1 5 10 15

Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
405 410 415

Leu

<210> 17
 <211> 1272
 <212> DNA
 <213> Homo sapiens

<400> 17
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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggc ctcagaaggc 240
 tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300
 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcattggat tcgccagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
 acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgcccc gacctttgct 480
 gactgggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tcctgtgagt ggccctcttta tatgtggccc tttcaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
 gggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840
 gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
 cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
 caggaccctt tgggcaagca agggtagcag cttagacagg gagacaactt tgaagtgtgg 1020
 gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggc 1080
 ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct 1140
 gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact 1200
 tcaagggtta gaagtcacat aaatcccaca ggcactgttt tgcttcagct atctgaaaag 1260
 gacgaattat ga 1272

<210> 18
 <211> 423
 <212> PRT

<213> Homo sapiens

<400> 18

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
1 5 10 15

Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn

<212> DNA
 <213> Homo sapiens

<400> 19
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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggc ctcagaaggc 240
 tgggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300
 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcattgggat tcgccagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
 acctgcgcag gcttcacctg gagttttgga tactacgaca ttgatgcca gacctttgct 480
 gactgggggag tagatctgct aaaatttgat gggtgttact gtgacagttt ggaaaatttg 540
 gcagatgggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tctgtgagt ggctcttta tatgtggccc tttcaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
 gggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840
 gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
 cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
 caggaccctt tgggcaagca agggtagcag cttagacagg gagacaactt tgaagtgtgg 1020
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 tcaagggttaa gataa 1215

<210> 20
 <211> 401
 <212> PRT
 <213> Homo sapiens

<400> 20

Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe Leu
 1 5 10 15

Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly
 20 25 30

Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met
 35 40 45

Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys
 50 55 60

Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp Lys Asp
 65 70 75 80

Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala Pro Gln
 85 90 95

Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe Pro His
 100 105 110

Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys Leu
 115 120 125

Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly
 130 135 140

Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly
 145 150 155 160

Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn
 165 170 175

Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg Thr Gly
 180 185 190

Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp Pro Phe
 195 200 205

Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His Trp Arg
 210 215 220

Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu
 225 230 235 240

Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro
 245 250 255

Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu
 260 265 270

Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala
 275 280 285

Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro Gln Ala
 290 295 300

Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln Asp Pro
 305 310 315 320

Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe Glu Val
 325 330 335

Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn
 340 345 350

Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser
 355 360 365

Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu
 370 375 380

Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu
 385 390 395 400

Arg

<210> 21
 <211> 1233
 <212> DNA
 <213> Homo sapiens

<400> 21
 atgcagctga ggaacccaga actacatctg ggctgcgcgc ttgcgcttcg cttcctggcc 60
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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggg ctcagaaggc 240

tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300
 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
 acctgcgag gcttccctgg gagttttgga tactacgaca ttgatgcccc gacctttgct 480
 gactggggag tagatctgct aaaatttgat ggttgttact gtgacagttt ggaaaatttg 540
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tcctgtgagt ggcctcttta tatgtggccc ttcaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
 ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840
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 cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
 caggaccctt tgggcaagca aggggtaccag cttagacagg gagacaactt tgaagtgtgg 1020
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 tcaagggttaa gatctgaaaa ggacgaatta tga 1233

<210> 22
 <211> 409
 <212> PRT
 <213> Homo sapiens

<400> 22

Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg
 1 5 10 15

Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp
 20 25 30

Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
 35 40 45

Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
 50 55 60

Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
65 70 75 80

Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
85 90 95

Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
100 105 110

Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu
115 120 125

Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
130 135 140

Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
145 150 155 160

Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
210 215 220

Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
245 250 255

Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
260 265 270

Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
275 280 285

Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
 290 295 300

Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln
 305 310 315 320

Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe
 325 330 335

Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met
 340 345 350

Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val
 355 360 365

Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr
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Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser
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Arg Leu Arg Ser Glu Lys Asp Glu Leu
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<400> 23

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Lys Asp Glu Leu
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Leu Gln Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu
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Gln Leu

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<400> 31

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